



147-199P.ST25.txt
SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Kufer, Peter
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<120> A novel method of identifying binding site domains that retain the capacity of binding to an epitope

<130> 147-199P

<140> US 09/554,465

<141> 2000-10-19

<150> PCT/EP98/07313

<151> 1998-11-16

<160> 71

<170> PatentIn version 3.0

<210> 1

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<213> artificial

<220>

<223> primer for human costimulatory protein CD80

<400> 1

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<212> DNA

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34

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<211> 36

<212> DNA

<213> artificial

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<223> primer for human CD80-M79scFv

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36

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<211> 37

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7-

1A antibody M74 V(L

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<211> 51

<212> DNA

<213> artificial

<220>

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7-

1A antibody M74 V(L

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<210> 6

<211> 96

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<213> artificial

<220>

<223> primer to single-chain Fv fragment (scFv) of the murine anti 17
-1

A antibody M74 V(H

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60

ctggtgaagc ctggggcttc agtgaagatt tcctgc
96

<210> 7
<211> 39
<212> DNA
<213> artificial

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<223> primer for the single-chain Fv fragment (scFv) of the murine anti-
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ti 17-1A antibody M74 V(H)

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60

atttcctgc
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<211> 64
<212> DNA
<213> artificial

<220>
<223> primer for single-chain Fv fragment (scFv) of the murine anti 1
7- 1A antibody M74 V(H)

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60

ccag
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<210> 10
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<212> DNA
<213> artificial

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<223> primer for single-chain Fv fragment (scFv) of the murine anti 1
7-
1A antibody M74 V(L

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17-1A antibody M74 V(L

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<210> 12
<211> 22
<212> DNA
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<220>
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<400> 12
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22

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<211> 17
<212> DNA
<213> artificial

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<220>
<223> primer for V(H) chain of human anti-17-1A antibody

<400> 13
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17

<210> 14
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<212> DNA
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<220>
<223> primer for V(L) chain of human anti-17-1A antibody

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38

<210> 15
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<223> primer for V(L) chain of human anti-17-1A antibody

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<210> 16
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<223> oligomer encoding six HIS residues

<400> 16
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<210> 17
<211> 24
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<220>

<223> oligomer containing six HIS residues

<400> 17

ctagtgtgat ggtgatggtg atgg

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<210> 18

<211> 47

<212> DNA

<213> artificial

<220>

<223> oligonucleotide for multiple cloning site containing SacI and X
ho

I overhang

<400> 18

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47

<210> 19

<211> 55

<212> DNA

<213> artificial

<220>

<223> oligonucleotide containing multiple cloning site with SacI and X
ho

I overhang

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55

<210> 20

<211> 79

<212> DNA

<213> artificial

<220>

<223> oligonucleotide containing multiple cloning sites

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ggtggttctg agctcggga

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gaggagacgg tgaccgggc
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<220>
 <223> primer for M13 gene III domain N2

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 29

<210> 23
 <211> 30
 <212> DNA
 <213> artificial

<220>
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<210> 24
 <211> 33
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<220>
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33

<210> 25
<211> 39
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<220>
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<210> 26
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<213> artificial

<220>
<223> primer for the extracellular region of the human CD54 antigen known as ICAM-

<400> 26
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32

<210> 27
<211> 30
<212> DNA
<213> artificial

<220>
<223> primer for the extracellular region of the human CD54 antigen known as ICAM-

<400> 27
gattccggac tcataccggg gggagagcac
30

<210> 28
<211> 30
<212> DNA

<213> artificial

<220>

<223> primer for the extracellular region of human CD58

<400> 28

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<210> 29

<211> 32

<212> DNA

<213> artificial

<220>

<223> primer for the extracellular region of human CD58

<400> 29

aagtcggat ctgtgtcttg aatgaccgct gc
32

<210> 30

<211> 32

<212> DNA

<213> artificial

<220>

<223> primer for the extracellular region of human CD86 costimulatory
p
rotei

<400> 30

aagtctagaa aatggatccc cagtgcacta tg
32

<210> 31

<211> 34

<212> DNA

<213> artificial

<220>

<223> primer for the extracellular region of human CD86 costimulatory
p
rotei

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34

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<220>
 <223> primers for murine V heavy chain

<400> 32
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 27

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<220>
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 gaggtccagc tgcagcagtc tggacct
 27

<210> 34
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<220>
 <223> primers for murine V heavy chain

<400> 34
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 27

<210> 35
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<220>
 <223> primers for murine V heavy chain

<400> 35
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 27

<210> 36
<211> 27
<212> DNA
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<220>
<223> primers for the murine V heavy chain

<400> 36
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27

<210> 37
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<212> DNA
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<220>
<223> primers for the murine V heavy chain

<400> 37
gaggtgaagc ttctcgagtc tggaggt
27

<210> 38
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<213> artificial

<220>
<223> primers for the murine V heavy chain

<400> 38
gaagtgaagc tcgaggagtc tggggga
27

<210> 39
<211> 27
<212> DNA
<213> artificial

<220>
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<400> 39
gaggttcagc tcgagcagtc tggagct
27

<210> 40
 <211> 34
 <212> DNA
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<220>
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<400> 40
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 34

<210> 41
 <211> 32
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 <213> artificial

<220>
 <223> primer for the murine V kappa chain

<400> 41
 ccagttccga gctcgttggtg actcaggaat ct
 32

<210> 42
 <211> 32
 <212> DNA
 <213> artificial

<220>
 <223> primer for the murine V kappa chain

<400> 42
 ccagttccga gctcgttggtg acgcagccgc cc
 32

<210> 43
 <211> 32
 <212> DNA
 <213> artificial

<220>
 <223> primer for the murine V kappa chain

<400> 43
 ccagttccga gctcgtgctc acccagtctc ca
 32

<210> 44
 <211> 32
 <212> DNA
 <213> artificial

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 <223> primer for the murine V kappa chain

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 32

<210> 45
 <211> 32
 <212> DNA
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 32

<210> 46
 <211> 32
 <212> DNA
 <213> artificial

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<400> 46
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 32

<210> 47
 <211> 32
 <212> DNA
 <213> artificial

<220>
 <223> primer for the murine V kappa gene

<400> 47
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 32

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<210> 48
<211> 38
<212> DNA
<213> artificial

<220>
<223> primer for the murine V kappa chain

<400> 48
tgggtgcacta gtcgtacgtt tgatctcaag cttggtcc
38

<210> 49
<211> 67
<212> DNA
<213> artificial

<220>
<223> oligonucleotide for the multiple cloning site

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60

cattgag
67

<210> 50
<211> 42
<212> DNA
<213> artificial

<220>
<223> sequence of the double-stranded oligonucleotide designated ACCG
S1
5BA

<400> 50
ccggagggtgg tggttccggg ggtggagggt caggcgggtgg tg
42

<210> 51
<211> 42
<212> DNA
<213> artificial

<220>
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M

<400> 51
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<210> 52
 <211> 14
 <212> PRT
 <213> artificial

<220>
 <223> peptide encoded by synthetic oligonucleotide

<400> 52
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
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<210> 53
 <211> 381
 <212> DNA
 <213> Homo sapiens

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 60

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 20

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 1
 80

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 2
 40

ctgcaaatac acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatatg 3
 00

gggtggggca gtggctggag accctactac tactacggta tggacgtctg gggccaaggg 3
 60

accacggtca ccgtctcctc a 3
 81

<210> 54
 <211> 321
 <212> DNA

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<213> Homo sapiens

<400> 54

gagctccaga tgacccagtc tccatcctcc ctgtctgctt ctgtgggaga cagagtcacc
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20

ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac 1
80

cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag tctacaacct 2
40

gaagattctg caacttacta ctgtcagcag agttacgaca tcccgtacac ttttggccag 3
00

gggaccaagc tggagatcaa a 3
21

<210> 55

<211> 201

<212> DNA

<213> artificial

<220>

<223> sequence designated L-F-NS3Frame (Figure 3.4)

<400> 55

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acaggtgtcc actccgacta caaagatgat gacgataagg atatcttcgg aggtgggtggt 1
20

agcgtattc catatggacg tcccgtcga ggctgtccat catcaccatc atcactgagc 1
80

ggccgctcta gagtcgacct c 2
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<210> 56

<211> 526

<212> DNA

<213> artificial

<220>

<223> M13-Phage and artificial sequence of the MCS

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20
cctaatacctt ctcttgagga gtctcagcct cttataactt tcatgtttca gaataatagg 1
80
ttccgaaata ggcagggggc attaactggt tatacgggca ctgttactca aggcactgac 2
40
cccgtaaaaa cttattacca gtacactcct gtatcatcaa aagccatgta tgacgcttac 3
00
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60
tgtgaatatc aaggccaatc gtctgacctg cctcaacctc ctgtcaatgc ttccggaggt 4
20
ggtggatccg aggtgcagct gctcgagccc ggtcaccgtc tctcaggtg gtggtgggtc 4
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26

<210> 57
<211> 726
<212> DNA
<213> Mus sp.

<400> 57
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atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 1
20
aggcctggac atggacttga gtggattgga gatcttttcc ctggaagtgg taataactcac 1
80
tacaatgaga gggtcagggg caaagccaca ctgactgcag acaaatactc gagcacagcc 2
40
tttatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 3
00
aggaactggg acgaggctat ggactactgg ggccaaggga ccacgggtcac cgtctcctca 3
60

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ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtcatgacc 4
20
cagtctccat cttatcttgc tgcattctct ggagaaacca ttactattaa ttgcagggca 4
80
agtaagagca ttagcaaata tttagcctgg tatcaagaga aacctgggaa aactaataag 5
40
cttcttatct actctggatc cactttgcaa tctggaattc catcaagggt cagtggcagt 6
00
ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcaatg 6
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atcaaa 7
26

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<210> 58
 <211> 753
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(753)

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act tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc aca agc
 96
 Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30

tat ggt tta agc tgg gtg aag cag aga act gga cag ggc ctt gag tgg 1
 44
 Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
 35 40 45

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tcc atg gag ctc cgc agc ctg aca tct gag gac tct gcg gtc tat ttc 88 Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe 85 90 95	2
tgt gca aga cgg gga tcc tac ggt agt aac tac gac tgg tac ttc gat 36 Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp 100 105 110	3
gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt 84 Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly 115 120 125	3
tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg acc 32 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr 130 135 140	4
cag act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc 80 Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile 145 150 155 160	4
tct tgc aga tct agt cag agc ctt gta cac agt aat gga aac acc tat	5

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28

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr

165

170

175

tta cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc

5

76

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

180

185

190

tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc

6

24

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly

195

200

205

agt gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct

6

72

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala

210

215

220

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac

7

20

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

225

230

235

240

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7

53

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

245

250

<210> 59

<211> 251

<212> PRT

<213> Mus sp.

<400> 59

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

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5

10

15

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			20					25					30		
Tyr	Gly	Leu	Ser	Trp	Val	Lys	Gln	Arg	Thr	Gly	Gln	Gly	Leu	Glu	Trp
		35					40					45			
Ile	Gly	Glu	Val	Tyr	Pro	Arg	Ile	Gly	Asn	Ala	Tyr	Tyr	Asn	Glu	Lys
	50					55					60				
Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala
65					70					75					80
Ser	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe
				85					90					95	
Cys	Ala	Arg	Arg	Gly	Ser	Tyr	Gly	Ser	Asn	Tyr	Asp	Trp	Tyr	Phe	Asp
			100					105					110		
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr
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Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile
145					150					155					160
Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr
				165					170					175	
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
			180					185					190		
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly
		195					200					205			
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala
	210					215					220				

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Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
245 250

<210> 60
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<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(726)

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Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly
1 5 10 15

act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac
96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg 1
44
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

att gga gat att tac cct gga agt ggt aat act cac tac aat gag agg 1
92
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc 2
40
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

147-199P.ST25.txt

ttt atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc 88 Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	2
85 90 95	
tgt gca aga ttg agg aac tgg gac gag cct atg gac tac tgg ggc caa 36 Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	3
100 105 110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc 84 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly	3
115 120 125	
ggc tcc ggt ggt ggt ggt tct gag ctc cag atg acc cag tct cca tct 32 Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser	4
130 135 140	
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca 80 Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala	4
145 150 155 160	
agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg 28 Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly	5
165 170 175	
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga 76 Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly	5
180 185 190	
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	6

147-199P.ST25.txt

24

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa
72

6

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210

215

220

cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag
20

7

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

225

230

235

240

atc aaa

26

Ile Lys

7

<210> 61

<211> 242

<212> PRT

<213> Mus sp.

<400> 61

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65		70		75		80
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	85			90		95
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	100			105		110
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly	115			120		125
Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser	130			135		140
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala	145			150		155
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly	165			170		175
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly	180			185		190
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	195			200		205
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln	210			215		220
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu	225			230		235
						240

Ile Lys

<210> 62
 <211> 744
 <212> DNA
 <213> Mus sp.

147-199P.ST25.txt

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<400> 62
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctggggac ttcagtgaag
60

atatcctgca aggcttctgg atacgccttc actaactact ggctagggtg ggttaagcag      1
20

aggcctggac atggacttga atgggttgga gatattttcc ctggaagtgg taatgctcac      1
80

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtcctc gtacacagcc      2
40

tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg      3
00

cggaactggg acgaggctat ggactactgg ggccaaggga ccacgggtcac cgtctcctca      3
60

ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca      4
20

cagtctccat cctccctgag tgtgtcagca ggagagaagg tcactatgag ctgcaagtcc      4
80

agtcagagtc tgtaaacag tggaaatcaa aagaactact tggcctggta ccagcagaaa      5
40

ccagggcagc ctctaaact gttgatctac ggggcatcca ctagggaatc tggggtcctt      6
00

gatcgcttca caggcagtgg atctggaaca gatttctctc tcaccatcag cagtgtgcag      6
60

gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgta cacgttcgga      7
20

ggggggacca agcttgagat caaa                                             7
44

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<210> 63
<211> 726
<212> DNA
<213> Mus sp.

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<220>
<221> CDS
<222> (1)..(726)

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<400> 63
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gtg agg cct ggg

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147-199P.ST25.txt

48

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1

5

10

15

gct tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc aat aac

96

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn

20

25

30

tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg

44

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

att gga gac att tac cct gga agt gga aat act cac tac aat gag agg

92

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg

50

55

60

ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc

40

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

ttt atg cag tta agt agc ctg aca tct gag gac tct gct gtc tat ttc

88

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

tgt gca aga ttg agg aac tgg gac gag gct atg gac tac tgg ggc caa

36

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc

84

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125	
ggc tcc ggt ggt ggt ggt tct gag ctc gtc atg acc cag tct cca tct			4
32			
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser			
130	135	140	
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca			4
80			
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala			
145	150	155	160
agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg			5
28			
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly			
165	170	175	
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga			5
76			
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly			
180	185	190	
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc			6
24			
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu			
195	200	205	
acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa			6
72			
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln			
210	215	220	
cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag			7
20			
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu			
225	230	235	240

atc aaa
26
Ile Lys

<210> 64
<211> 242
<212> PRT
<213> Mus sp.

<400> 64

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
Page 29

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44

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp

35

40

45

att gga gag gtt tat cct aga att ggt aat gct tac tac aat gag aag

1

92

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys

50

55

60

ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcg

2

40

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

tcc atg gag ctc cgc agc ctg acc tct gag gac tct gcg gtc tat ttc

2

88

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

tgt gca aga cgg gga tcc tac gat act aac tac gac tgg tac ttc gat

3

36

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp

100

105

110

gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt

3

84

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg acc

4

32

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr

130

135

140

cag act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc

4

80

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile

145	150	155	160	
tct tgc aga tct agt cag agc ctt gta cac agt aat gga aac acc tat				5
28				
Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr				
	165	170	175	
tta cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc				5
76				
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
	180	185	190	
tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc				6
24				
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly				
	195	200	205	
agt gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct				6
72				
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala				
	210	215	220	
gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac				7
20				
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr				
225	230	235	240	
acg ttc gga ggg ggg acc aag ctt gag atc aaa				7
53				
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys				
	245	250		

<210> 66
 <211> 251
 <212> PRT
 <213> Mus sp.

<400> 66

147-199P.ST25.txt

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly		
1				5					10					15			
Ala	Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn		
			20					25					30				
Tyr	Gly	Leu	Ser	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Val	Leu	Glu	Trp		
		35					40					45					
Ile	Gly	Glu	Val	Tyr	Pro	Arg	Ile	Gly	Asn	Ala	Tyr	Tyr	Asn	Glu	Lys		
	50					55					60						
Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala		
65					70					75					80		
Ser	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe		
				85					90					95			
Cys	Ala	Arg	Arg	Gly	Ser	Tyr	Asp	Thr	Asn	Tyr	Asp	Trp	Tyr	Phe	Asp		
			100					105					110				
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly		
		115					120					125					
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr		
	130					135					140						
Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile		
145					150					155					160		
Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr		
				165					170					175			
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile		
			180					185					190				
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly		
		195					200					205					

147-199P.ST25.txt

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
210 215 220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
245 250

<210> 67
<211> 717
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(717)

<400> 67
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48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt aga tac
96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa tgg att 1
44
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

gga gaa att aat cca gat agc agt acg ata aac tat acg cca tct ctg 1
92
Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg ctg tac 2
Page 34

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40

Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr

65

70

75

80

ctg caa atg ggc aaa gtg aga tct gag gac aca gcc ctt tat tac tgt 2

88

Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys

85

90

95

gca aga gga gcc ttc ctt ttt gac tac tgg ggc caa ggg acc acg gtc 3

36

Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val

100

105

110

acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc ggc tcc ggt ggt 3

84

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

115

120

125

ggt ggt tct gag ctc gtg ctc acc cag tct cca acc acc atg gct gca 4

32

Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala

130

135

140

tct ccc ggg gag aag atc act atc acc tgc agt gcc agc tca agt ata 4

80

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile

145

150

155

160

agt tcc aat tac ttg cat tgg tat cag cag aag cca gga ttc tcc cct 5

28

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro

165

170

175

aaa ctc ttg att tat agg aca tcc aat ctg gct tct gga gtc cca gct 5

76

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala

180

185

190

cgc ttc agt ggc agt ggg tct ggg acc tct tac tct ctc aca att ggc 6
24

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly

195

200

205

acc atg gag gct gaa gat gtt gcc act tac tac tgc cag cag ggt agt 6
72

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser

210

215

220

agt ata cca ctc acg ttc ggt gct ggg acc aag ctt gag atc aaa 7
17

Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys

225

230

235

<210> 68
<211> 239
<212> PRT
<213> Mus sp.

<400> 68

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

147-199P.ST25.txt

Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
130 135 140

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
145 150 155 160

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
165 170 175

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
195 200 205

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser
210 215 220

Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 69
<211> 744
<212> DNA
<213> Mus sp.

<400> 69
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctgggac ttcagtgaag
60

atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag
20

1

147-199P.ST25.txt

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aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 1
80

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 2
40

tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 3
00

aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 3
60

ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 4
20

cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 4
80

agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 5
40

ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 6
00

gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 6
60

gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 7
20

gctgggacca agcttgagat caaa 7
44

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<210> 70
<211> 744
<212> DNA
<213> Mus sp.

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<220>
<221> CDS
<222> (1)..(744)

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<400> 70
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg
48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

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act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac
Page 38

```

147-199P.ST25.txt

96

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

tac tgg cta ggt tgg gtt aag cag agg cct gga cat gga ctt gaa tgg

1

44

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

gtt gga gat att ttc cct gga agt ggt aat gct cac tac aat gag aag

1

92

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys

50

55

60

ttc aag ggc aaa gcc aca ctg act gca gac aag tcc tcg tac aca gcc

2

40

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala

65

70

75

80

tat atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc

2

88

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

tgt gca aga ttg cgg aac tgg gac gag gct atg gac tac tgg ggc caa

3

36

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc

3

84

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc

4

32

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

135

140

tcc ctg gct atg tca gta gga cag aag gtc act atg agc tgc aag tcc 4
80

Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser

145

150

155

160

agt cag agc ctt tta aat agt agc aat caa aag aac tat ttg gcc tgg 5
28

Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp

165

170

175

tac cag cag aaa caa ggg cag cct cct aaa ctg ctt atc tat ggg gca 5
76

Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala

180

185

190

tcc att aga gaa tct tgg gtc cct gat cga ttc aca gga agt gga tct 6
24

Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser

195

200

205

ggg aca gac ttc act ctc acc atc agc agt gtg aag gct gaa gac ctg 6
72

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu

210

215

220

gca gtt tat tac tgt cag caa tat tat agc tat ccg tac acg ttc gga 7
20

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly

225

230

235

240

ggg ggg acc aag ctt gag atc aaa 7
44

Gly Gly Thr Lys Leu Glu Ile Lys

245

147-199P.ST25.txt

<210> 71
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 71

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Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
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Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
 165 170 175

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Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala
 180 185 190

Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly
 225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys
 245